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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/922,067

DATE: 12/19/2001
TIME: 12:34:19

Input Set : N:\Crf3\RULE60\09922067.txt
Output Set: N:\CRF3\12192001\I922067.raw

SEQUENCE LISTING

```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: MacPhee, Colin Houston
 6                    Tew, David Graham
 7                    Southan, Christopher Donald
 8                    Hickey, Dierdre Mary Bernadette
 9                    Gloger, Israel Simon
10                    Lawrence, Geoffrey Mark Prouse
11                    Rice, Simon Quentyn John
13     (ii) TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
14                             Thereof And Use Of The Same In Diagnosis And Therapy
16    (iii) NUMBER OF SEQUENCES: 11
18     (iv) CORRESPONDENCE ADDRESS:
19          (A) ADDRESSEE: SmithKline Beecham Corporation
20          (B) STREET: 709 Swedeland Road
21          (C) CITY: King of Prussia
22          (D) STATE: PA
23          (E) COUNTRY: USA
24          (F) ZIP: 19406
26      (v) COMPUTER READABLE FORM:
27          (A) MEDIUM TYPE: Diskette
28          (B) COMPUTER: IBM PC compatible
29          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
32     (vi) CURRENT APPLICATION DATA:
```
C--> 33 `          (A) APPLICATION NUMBER: US/09/922,067`
C--> 34 `          (B) FILING DATE: 03-Aug-2001`
```
35          (C) CLASSIFICATION:
37    (vii) PRIOR APPLICATION DATA:
38          (A) APPLICATION NUMBER: 09/193,130
39          (B) FILING DATE: 1998-11-17
41          (A) APPLICATION NUMBER: PCT/GB94/01374
42          (B) FILING DATE: 24 June 1994
44   (viii) ATTORNEY/AGENT INFORMATION:
45          (A) NAME: Dustman, Wayne J.
46          (B) REGISTRATION NUMBER: 33,870
47          (C) REFERENCE/DOCKET NUMBER: P30693
49     (ix) TELECOMMUNICATION INFORMATION:
50          (A) TELEPHONE: 610-270-5023
51          (B) TELEFAX: 610-270-5090
52          (C) TELEX:
54 (2) INFORMATION FOR SEQ ID NO: 1:
56      (i) SEQUENCE CHARACTERISTICS:
57          (A) LENGTH: 37 amino acids
58          (B) TYPE: amino acid
59          (C) STRANDEDNESS:
60          (D) TOPOLOGY: linear
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Output Set: **N:\CRF3\12192001\I922067.raw**

```
62        (ii) MOLECULE TYPE: peptide
64       (iii) HYPOTHETICAL: NO
C--> 68        (v) FRAGMENT TYPE: internal
70       (vi) ORIGINAL SOURCE:
C--> 72       (ix) FEATURE:
74       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76        Met Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Ala Ala Ile Asp Leu
77        1               5               10              15
79        Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His
80                    20              25              30
82        Lys Asp Phe Asp Gln
83                    35
85  (2) INFORMATION FOR SEQ ID NO: 2:
87        (i) SEQUENCE CHARACTERISTICS:
88            (A) LENGTH: 30 amino acids
89            (B) TYPE: amino acid
90            (D) TOPOLOGY: linear
92       (ii) MOLECULE TYPE: peptide
94      (iii) HYPOTHETICAL: NO
96        (v) FRAGMENT TYPE: internal
100      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
102       Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro
103       1               5               10              15
105       Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn
106                   20              25              30
108  (2) INFORMATION FOR SEQ ID NO: 3:
110       (i) SEQUENCE CHARACTERISTICS:
111           (A) LENGTH: 27 amino acids
112           (B) TYPE: amino acid
113           (D) TOPOLOGY: linear
115      (ii) MOLECULE TYPE: peptide
117     (iii) HYPOTHETICAL: NO
119       (v) FRAGMENT TYPE: internal
123      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
125       Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His
126       1               5               10              15
128       Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
129                   20              25
131  (2) INFORMATION FOR SEQ ID NO: 4:
133       (i) SEQUENCE CHARACTERISTICS:
134           (A) LENGTH: 19 amino acids
135           (B) TYPE: amino acid
136           (D) TOPOLOGY: linear
138      (ii) MOLECULE TYPE: peptide
140     (iii) HYPOTHETICAL: NO
142       (v) FRAGMENT TYPE: internal
146      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
148       Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
149       1               5               10              15
```

```
151      Pro Ala Asn
154 (2) INFORMATION FOR SEQ ID NO: 5:
156      (i) SEQUENCE CHARACTERISTICS:
157          (A) LENGTH: 420 base pairs
158          (B) TYPE: nucleic acid
159          (C) STRANDEDNESS: double
160          (D) TOPOLOGY: linear
162      (ii) MOLECULE TYPE: cDNA
164      (iii) HYPOTHETICAL: NO
C--> 166     (iv) ANTI-SENSE: NO
170      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
172 AAAAAACCTA TTTTAATCCT AATTGTATTT CTCTATTCCT GAAGAGTTCT GTAACATGAT    60
174 GTGTTGATTG GTTGTGTTAA TGTTGGTCCC TGGAATAAGA TTCTCATCAT CTCCTTCAAT   120
176 CAAGCAGTCC CACTGATCAA AATCTTTATG AAGTCCTAAA TGCTTTTGTA AGAATGCTAA   180
178 TGAAGCTTTG TTGCTAAGAT CAATAGCTGC ATTTGAATCT ATGTCTCCCT TTAATTTGAG   240
180 CATGTGTCCA ATTATTTTGC CAGTNGCAAA AGTGAAGTCA GCAAAATTCT GGTGGACTGA   300
182 ACCCCTGATT GTAATCATCT TTCTTTCTTT ATCAGGTGAG TAGCATTTTT TCATTTTTAT   360
184 GATATTAGCA GGATATTGGA AATATTCAGN GTTGNTAAAA AGNGGNGGCT GAGGGATTCT   420
187 (2) INFORMATION FOR SEQ ID NO: 6:
189      (i) SEQUENCE CHARACTERISTICS:
190          (A) LENGTH: 379 base pairs
191          (B) TYPE: nucleic acid
192          (C) STRANDEDNESS: double
193          (D) TOPOLOGY: linear
195      (ii) MOLECULE TYPE: cDNA
197      (iii) HYPOTHETICAL: NO
C--> 199     (iv) ANTI-SENSE: NO
203      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
205 TGCTAATATC ATAAAAATGA AAAAATGCTA CTCACCTGAT AAAGAAAGAA AGATGATTAC    60
207 AATCAGGGGT TCAGTCCACC AGANTTTTGC TGACTTCACT TTTGCAACTG GCAAAATAAT   120
209 TGGACACATG CTCAAATTAA AGGGAGACAT AGATTCAAAT GTAGCTATTG ATCTTAGCAA   180
211 CAAAGCTTCA TTAGCATTCT TACAAAAGCA TTTAGGACTT CATAAAGATT TTGTTCAGTG   240
213 GGACTGCTTG ATTGAAGGAG ATGATGAGAA TCTTATTCCA GGGACCAACA TTAACACAAC   300
215 CAATTCAACA CATCATGTTT ACAGAACTTC TTCCAGGGAA TAGGAGGAAA TACAATTGGG   360
217 GTTTAAAATA GGTTTTTTT                                               379
219 (2) INFORMATION FOR SEQ ID NO: 7:
221      (i) SEQUENCE CHARACTERISTICS:
222          (A) LENGTH: 279 base pairs
223          (B) TYPE: nucleic acid
224          (C) STRANDEDNESS: double
225          (D) TOPOLOGY: linear
227      (ii) MOLECULE TYPE: cDNA
229      (iii) HYPOTHETICAL: NO
C--> 231     (iv) ANTI-SENSE: NO
235      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
237 GAAGAATGCA TTAGATTTAA AGTTTGATAT GGAACAACTG AAGGACTCTA TTGATAGGGA    60
239 AAAAATAGCA GTAATTGGAC ATTCTTTTGG TGGAGCAACG GTTATTCAGA CTCTTAGTGA   120
241 AGATCAGAGA TTCAGATGTG GTATTGCCCT GGATGCATGG ATGTTTCCAC TGGGTGATGA   180
243 AGTATATTCC AGAATTCCTC AGCCCCTCTT TTTTATCAAC TCTGAATATT TCCAATATCC   240
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245 TGCTAATATC ATAAAANTGG AAAAATGCTA CTCACCTGG                        279
247 (2) INFORMATION FOR SEQ ID NO: 8:
249     (i) SEQUENCE CHARACTERISTICS:
250           (A) LENGTH: 572 base pairs
251           (B) TYPE: nucleic acid
252           (C) STRANDEDNESS: double
253           (D) TOPOLOGY: linear
255     (ii) MOLECULE TYPE: cDNA
257     (iii) HYPOTHETICAL: NO
259     (iv) ANTI-SENSE: NO                                  C-->
263     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
265 AAAATAGCAG TAATTGGACA TTCTTTAGGT GGAGCAACGG TTATTCAGAC TCTTAGTGAA   60
267 GATCAGAGAT TCAGATGTGG TATTGCCCTG GATGCATGGA TGTTTCCACT GGGTGATGAA  120
269 GTATATTCCA GAATTCCTCA GCCCCTCTTT TTTATCAACT CTGAATATTT CCAATATCCT  180
271 GCTAATATCA TAAAAATGAA AAAATGCTAC TCACCTGATA AAGAAAGAAA GATGATTACA  240
273 ATCAGGGGTT CAGTCCACCA GAATTTTGCT GACTTCACTT TTGCAACTGG CAAAATAATT  300
275 GGACACATGC TCAAATTAAA GGGAGACATA GATTCAAATG TAGCTATTGA TCTTAGCAAC  360
277 AAAGCTTCAT CAGCATTCTT ACAAAAGCAT TTAGGACTTC ATAAAGATTT TGATCAGTGG  420
279 GACTGCTTGA TTGAAGGAGA TGATGAGAAT CTTATTCCAG GGACCAACAT TAACACAACC  480
281 AATCAACACA TCATGTTACA GAACTCTTCA GGAATAGAGA AATACAATTA GGATTAAAAT  540
283 AGGTTTTTTA AAAAAAAAAA AAAAAAACT CG                                 572
285 (2) INFORMATION FOR SEQ ID NO: 9:
287     (i) SEQUENCE CHARACTERISTICS:
288           (A) LENGTH: 1361 base pairs
289           (B) TYPE: nucleic acid
290           (C) STRANDEDNESS: double
291           (D) TOPOLOGY: linear
293     (ii) MOLECULE TYPE: cDNA
295     (iii) HYPOTHETICAL: NO
297     (iv) ANTI-SENSE: NO                                  C-->
300     (ix) FEATURE:
301           (A) NAME/KEY: CDS
302           (B) LOCATION: 38..1360
305     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
307 TGAGAGACTA AGCTGAAACT GCTGCTCAGC TCCCAAG ATG GTG CCA CCC AAA TTG    55
308                                             Met Val Pro Pro Lys Leu
309                                              1                   5
311 CAT GTG CTT TTC TGC CTC TGC GGC TGC CTG GCT GTG GTT TAT CCT TTT    103
312 His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
313             10                  15                  20
315 GAC TGG CAA TAC ATA AAT CCT GTT GCC CAT ATG AAA TCA TCA GCA TGG    151
316 Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
317         25                  30                  35
319 GTC AAC AAA ATA CAA GTA CTG ATG GCT GCT GCA AGC TTT GGC CAA ACT    199
320 Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
321     40                  45                  50
323 AAA ATC CCC CGG GGA AAT GGG CCT TAT TCC GTT GGT TGT ACA GAC TTA    247
324 Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
325 55                  60                  65                  70
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327 ATG TTT GAT CAC ACT AAT AAG GGC ACC TTC TTG CGT TTA TAT TAT CCA        295
328 Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro
329                 75                  80                  85
331 TCC CAA GAT AAT GAT CGC CTT GAC ACC CTT TGG ATC CCA AAT AAA GAA        343
332 Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu
333                 90                  95                 100
335 TAT TTT TGG GGT CTT AGC AAA TTT CTT GGA ACA CAC TGG CTT ATG GGC        391
336 Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly
337             105                 110                 115
339 AAC ATT TTG AGG TTA CTC TTT GGT TCA ATG ACA ACT CCT GCA AAC TGG        439
340 Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp
341     120                 125                 130
343 AAT TCC CCT CTG AGG CCT GGT GAA AAA TAT CCA CTT GTT GTT TTT TCT        487
344 Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser
345 135                 140                 145                 150
347 CAT GGT CTT GGG GCA TTC AGG ACA CTT TAT TCT GCT ATT GGC ATT GAC        535
348 His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp
349                 155                 160                 165
351 CTG GCA TCT CAT GGG TTT ATA GTT GCT GCT GTA GAA CAC AGA GAT AGA        583
352 Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg
353             170                 175                 180
355 TCT GCA TCT GCA ACT TAC TAT TTC AAG GAC CAA TCT GCT GCA GAA ATA        631
356 Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile
357             185                 190                 195
359 GGG GAC AAG TCT TGG CTC TAC CTT AGA ACC CTG AAA CAA GAG GAG GAG        679
360 Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu
361     200                 205                 210
363 ACA CAT ATA CGA AAT GAG CAG GTA CGG CAA AGA GCA AAA GAA TGT TCC        727
364 Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser
365 215                 220                 225                 230
367 CAA GCT CTC AGT CTG ATT CTT GAC ATT GAT CAT GGA AAG CCA GTG AAG        775
368 Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys
369             235                 240                 245
371 AAT GCA TTA GAT TTA AAG TTT GAT ATG GAA CAA CTG AAG GAC TCT ATT        823
372 Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile
373             250                 255                 260
375 GAT AGG GAA AAA ATA GCA GTA ATT GGA CAT TCT TTT GGT GGA GCA ACG        871
376 Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr
377             265                 270                 275
379 GTT ATT CAG ACT CTT AGT GAA GAT CAG AGA TTC AGA TGT GGT ATT GCC        919
380 Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala
381     280                 285                 290
383 CTG GAT GCA TGG ATG TTT CCA CTG GGT GAT GAA GTA TAT TCC AGA ATT        967
384 Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile
385 295                 300                 305                 310
387 CCT CAG CCC CTC TTT TTT ATC AAC TCT GAA TAT TTC CAA TAT CCT GCT       1015
388 Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala
389             315                 320                 325
391 AAT ATC ATA AAA ATG AAA AAA TGC TAC TCA CCT GAT AAA GAA AGA AAG       1063
```

VERIFICATION SUMMARY   DATE: 12/19/2001
PATENT APPLICATION: **US/09/922,067**   TIME: 12:34:20

            Input Set : **N:\Crf3\RULE60\09922067.txt**
            Output Set: **N:\CRF3\12192001\I922067.raw**

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:66 M:220 C: Keyword misspelled or invalid format, [(v) FRAGMENT TYPE:]
L:72 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:166 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:199 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:231 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:259 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:297 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]